Detailed analyses of 12 hom(oe)ologous chromosome segments in the highly polyploid sugarcane genome

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Modern sugarcane cultivars (*Saccharum* spp.) are recognized as the crop with the most complex genome studied to date, mainly due to the very high level of vertical redundancy (2n = ca 12x = ca 120), together with an interspecific origin. They are derived from hybridization, performed by breeders a century ago, between two autopolyploid species, namely *S. officinarum* (domesticated) and *S. spontaneum* (wild species, 2n=5x=40 to 16x=128). To investigate the impact of polyploidization on its genome organization and more widely on its performance and plasticity, we finely analyzed the structural organization of hom(oe)ologous chromosomes. Thirty-three homoeologous BAC clones from four regions of the sugarcane R570 genome were identified, sequenced, finely annotated and compared, representing more than 3 Mb of sugarcane DNA sequence.

For all four regions, almost perfect gene colinearity and high gene structure and sequence conservation were observed, confirming previous preliminary analyses on two of these regions. Moreover, the vast majority of the homoeologous genes were predicted, based on their structure, to be functional and showed signs of evolving under purifying selection. For one of the region carrying the *Adh1* gene, we extended the homoeologous series to 13 hom(oe)ologous chromosome segments.

Gene similarity and patterns of transposable element insertions are currently being analyzed in order to determine the origin (*S. officinarum vs S. spontaneum*) and the evolutionary dynamics of these hom(oe)ologous regions.

Homoeologous alleles, bacterial artificial chromosome (BAC) sequence, sugarcane, gene conservation, *Adh1* locus